

Package: flexMatch (via r-universe)

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Description What the package does (one paragraph).
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assess_match_quality	<i>Assess Matching Quality (Academic Standard)</i>
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Description

Assess Matching Quality (Academic Standard)

Usage

```
assess_match_quality(  
  match_res,  
  stack_candidates,  
  dt,  
  match_vars,  
  id_col,  
  time_col  
)
```

expand_matched_stacks	<i>Expand Matched Cross-Section to Full Stacks</i>
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Description

Expand Matched Cross-Section to Full Stacks

Usage

```
expand_matched_stacks(  
  dt,  
  matched_data,  
  id_col,  
  time_col,  
  k_pre,  
  k_post,  
  match_by = -1  
)
```

flexmatch

*Flexmatch: The All-in-One Stacked DiD Wrapper***Description**

Orchestrates the entire Stacked DiD pipeline: Scans candidates, Matches them, Expands to stacks, Assesses Quality, and Visualizes Events.

Usage

```
flexmatch(
  dt,
  id_col,
  time_col,
  event_col,
  k_pre,
  k_post,
  k_freeze,
  match_vars,
  match_by = -1,
  assess_quality = TRUE,
  plot_events = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

<code>dt</code>	The original panel data (data.table).
<code>id_col</code>	Character. Name of ID column.
<code>time_col</code>	Character. Name of time column (integer/numeric).
<code>event_col</code>	Character. Name of event dummy (1 = start of treatment).
<code>k_pre</code>	Integer. Required pre-periods.
<code>k_post</code>	Integer. Required post-periods.
<code>k_freeze</code>	Integer. Freeze/Cool-down periods after <code>k_post</code> .
<code>match_vars</code>	Character vector. Covariates to match on.
<code>match_by</code>	Integer. Relative period for matching (default -1).
<code>assess_quality</code>	Logical. If TRUE, runs balance checks. Default TRUE.
<code>plot_events</code>	Logical. If TRUE, runs the event dynamics plot. Default TRUE.
<code>verbose</code>	Logical. If TRUE, prints progress. Default TRUE.
<code>...</code>	Additional arguments passed directly to MatchIt (e.g., <code>ratio</code> , <code>method</code> , <code>replace</code> , <code>caliper</code>).

Value

- A list containing:
- final_expanded_data: The analysis-ready stacked dataset.
 - matched_cross_section: The matched pairs at time t.
 - stack_candidates: The full pool of eligible units.
 - quality_stats: List with Balance Table and Density Plots.
 - event_plot: The Lasagna plot object.
 - match_object: The raw MatchIt model.

label_candidates	<i>Label Treatment and Control Stack Candidates</i>
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Description

Identifies valid stack candidates by enforcing strict data continuity and clean history/future constraints.

Usage

```
label_candidates(  
  dt,  
  id_col,  
  time_col,  
  event_col,  
  k_pre,  
  k_post,  
  k_freeze,  
  match_by = -1  
)
```

match_candidates	<i>Cross-Sectional Matching for Stacked DiD</i>
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Description

Performs exact cohort matching + 1-to-K matching using MatchIt.

Usage

```
match_candidates(dt, stack_candidates, id_col, time_col, match_vars, ...)
```

plot_event_dynamics	<i>Plot Event Dynamics (Lasagna Plot with Overlay)</i>
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Description

Plot Event Dynamics (Lasagna Plot with Overlay)

Usage

```
plot_event_dynamics(  
  dt,  
  dt_matched = NULL,  
  id_col,  
  time_col,  
  event_col,  
  n_bins = 4L,  
  sort_by_intensity = FALSE  
)
```

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